

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/026,459ADATE: 11/18/98  
TIME: 15:17:21

INPUT SET: S29925.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Xu, Hong-Ji  
Hu, Shi-Xue  
Benedict, William F.  
Zhou, Yunli

(ii) TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR  
PROTEINS

(iii) NUMBER OF SEQUENCES: 51

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Arnold, White & Durkee  
(B) STREET: P.O. Box 4433  
(C) CITY: Houston  
(D) STATE: TX  
(E) COUNTRY: USA  
(F) ZIP: 77210-4433

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US UNKNOWN  
(B) FILING DATE: 19-FEB-1998  
(C) CLASSIFICATION: UNKNOWN

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/038,118  
(B) FILING DATE: 20-FEB-1997

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hibler, David W.  
(B) REGISTRATION NUMBER: 41,071  
(C) REFERENCE/DOCKET NUMBER: UTXC:506

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 512/418-3000  
(B) TELEFAX: 512/474-7577

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/026,459A

 DATE: 11/18/98  
 TIME: 15:17:22

INPUT SET: S29925.raw

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47
48 (2) INFORMATION FOR SEQ ID NO:1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 3555 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
55
56 (ix) FEATURE:
57 (A) NAME/KEY: CDS
58 (B) LOCATION: 7..2790
59
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62 CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC      48
63 Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala
64 1 5 10
65
66 GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG      96
67 Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu
68 15 20 25 30
69
70 GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG      144
71 Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg
72 35 40 45
73
74 CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG      192
75 Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln
76 50 55 60
77
78 AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG      240
79 Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp
80 65 70 75
81
82 GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG      288
83 Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys
84 80 85 90
85
86 AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA      336
87 Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu
88 95 100 105 110
89
90 GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC      384
91 Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile
92 115 120 125
93
94 AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC      432
95 Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr
96 130 135 140
97
98 AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG      480
99 Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu
  
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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/026,459A

DATE: 11/18/98  
TIME: 15:17:24

INPUT SET: S29925.raw

100	145	150	155	
101				
102	TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG			528
103	Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu			
104	160	165	170	
105				
106	ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG			576
107	Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val			
108	175	180	185	190
109				
110	CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA			624
111	Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu			
112		195	200	205
113				
114	CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC			672
115	Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val			
116		210	215	220
117				
118	CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA			720
119	Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro			
120		225	230	235
121				
122	TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG			768
123	Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg			
124		240	245	250
125				
126	CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT			816
127	Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp			
128		255	260	265
129				270
130	ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT			864
131	Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp			
132		275	280	285
133				
134	GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT			912
135	Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser			
136		290	295	300
137				
138	CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT			960
139	Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser			
140		305	310	315
141				
142	AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA			1008
143	Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg			
144		320	325	330
145				
146	TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT			1056
147	Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser			
148		335	340	345
149				350
150	TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG			1104
151	Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val			
152		355	360	365

DATE: 11/18/98  
TIME: 15:17:26

**INPUT SET: S29925.raw**

153																	
154	AAT	GTA	ATT	CCT	CCA	CAC	ACT	CCA	GTT	AGG	ACT	GTT	ATG	AAC	ACT	ATC	1152
155	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	
156				370				375						380			
157																	
158	CAA	CAA	TTA	ATG	ATG	ATT	TTA	AAT	TCA	GCA	AGT	GAT	CAA	CCT	TCA	GAA	1200
159	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	
160				385				390						395			
161																	
162	AAT	CTG	ATT	TCC	TAT	TTT	AAC	AAC	TGC	ACA	GTG	AAT	CCA	AAA	GAA	AGT	1248
163	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	
164				400				405						410			
165																	
166	ATA	CTG	AAA	AGA	GTG	AAG	GAT	ATA	GGA	TAC	ATC	TTT	AAA	GAG	AAA	TTT	1296
167	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	
168				415				420						425			430
169																	
170	GCT	AAA	GCT	GTG	GGA	CAG	GGT	TGT	GTC	GAA	ATT	GGA	TCA	CAG	CGA	TAC	1344
171	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	
172				435				440						445			
173																	
174	AAA	CTT	GGA	GTT	CGC	TTG	TAT	TAC	CGA	GTA	ATG	GAA	TCC	ATG	CTT	AAA	1392
175	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	
176				450				455						460			
177																	
178	TCA	GAA	GAA	GAA	CGA	TTA	TCC	ATT	CAA	AAT	TTT	AGC	AAA	CTT	CTG	AAT	1440
179	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	
180				465				470						475			
181																	
182	GAC	AAC	ATT	TTT	CAT	ATG	TCT	TTA	TTG	GCG	TGC	GCT	CTT	GAG	GTT	GTA	1488
183	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	
184				480				485						490			
185																	
186	ATG	GCC	ACA	TAT	AGC	AGA	AGT	ACA	TCT	CAG	AAT	CTT	GAT	TCT	GGA	ACA	1536
187	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	
188				495				500						505			510
189																	
190	GAT	TTG	TCT	TTC	CCA	TGG	ATT	CTG	AAT	GTG	CTT	AAT	TTA	AAA	GCC	TTT	1584
191	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	
192				515				520						525			
193																	
194	GAT	TTT	TAC	AAA	GTG	ATC	GAA	AGT	TTT	ATC	AAA	GCA	GAA	GGC	AAC	TTG	1632
195	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	
196				530				535						540			
197																	
198	ACA	AGA	GAA	ATG	ATA	AAA	CAT	TTA	GAA	CGA	TGT	GAA	CAT	CGA	ATC	ATG	1680
199	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	
200				545				550						555			
201																	
202	GAA	TCC	CTT	GCA	TGG	CTC	TCA	GAT	TCA	CCT	TTA	TTT	GAT	CTT	ATT	AAA	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/026,459A

DATE: 11/18/98  
TIME: 15:17:27

INPUT SET: S29925.raw

206	CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT	1776
207	Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys	
208	575 580 585 590	
209		
210	CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT	1824
211	Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr	
212	595 600 605	
213		
214	CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA	1872
215	Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val	
216	610 615 620	
217		
218	AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1920
219	Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
220	625 630 635	
221		
222	CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1968
223	Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	
224	640 645 650	
225		
226	TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG	2016
227	Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu	
228	655 660 665 670	
229		
230	TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	2064
231	Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His	
232	675 680 685	
233		
234	ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA	2112
235	Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln	
236	690 695 700	
237		
238	ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC	2160
239	Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp	
240	705 710 715	
241		
242	CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT	2208
243	Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala	
244	720 725 730	
245		
246	GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT	2256
247	Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp	
248	735 740 745 750	
249		
250	TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA	2304
251	Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr	
252	755 760 765	
253		
254	AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA	2352
255	Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile	
256	770 775 780	
257		
258	CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG	2400

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
PATENT APPLICATION *US/09/026,459A*

DATE: 11/18/98  
TIME: 15:17:29

*INPUT SET: S29925.raw*

Line	Error	Original Text
30	Wrong application Serial Number	(A) APPLICATION NUMBER: US UNKNOWN
32	Wrong Classification	(C) CLASSIFICATION: UNKNOWN